Q823p2 chlamydophi Q9pkb6 chlamydia m Q928b6 chlamydia t G84280 chlamydia t C6meh4 parachlamyd G273025 parachlamyd Q9vhv2 drosophila Q86nz3 drosophila Q86nz3 drosophila Q9tt07 canis famil Q9tt07 canis famil Q9t673 pseudomonas Q9tun3 plaamid psb O91un3 plaamid psb

OM protein

6

Run

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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids I; Fabales, Fabaceae, Papilionoideae, Phaseoleae, Glycine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
TISSUE-Cotyledon;
Adachi M., Kateube T., Masuda T., Utsumi S.;
Adachi M., Kateube T., Masuda T., Utsumi S.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
-!-SIBUNIT: Haxamer; each subunit is composed of an acidic and a basic chain derived from a single precursor and linked by a disulfide bond (By similarity).
-!- SIMILARITY: Belongs to the 11S seed storage protein (globulins)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q39922 PRELIMINARY; PRT; 517 AA.
Q39922;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Gy5 protein.
Name=Gy5;
Name=Gy5;
Glycine soja (Wild soybean).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AB04940; BAB15802.1; -.
InterPro; IPR006045; Cupin.
InterPro; IPR01113; Cupin.
InterPro; IPR011051; RmLC_like_cupin.
InterPro; IPR011051; RmLC_like_cupin.
InterPro; IPR006044; Seedstore_lis.
PRIMTS; PR00439; 11SGLOBULIN.
PROSITE; PS00305; 11S_SEDS_STORAGE; 1.
Seed storage protein; Scorage protein.
SeeQUENCE 517 AA; 58187 MW; 0440F44C72181B7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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100.0%; Pred. No. 0.71;
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NORB_CHLCV
NORB_CHLMU
NORB_CHLMU
NORB_CHLTR
NORB_CHLTR
CAE33025
CAEMEH4
CAE33025
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CAE3102
OGST10
OGST14
OGST14
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Best Local Similarity luv...
Best Local Similarity
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||PPGVPYWT 157
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05-JUL-2004
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   149
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Q7GC77
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O46604 sus scrofa
O9nuj7 homo sapien
Q63241 rattus norv
Q63239 rattus norv
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                                                                                                                  Search time 120.375 Seconds (without alignments) 43.019 Million cell updates/sec
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                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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Q8PLJ6
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Q9S9D0
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1: uniprot_sprot:*
2: uniprot_trembl:*
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seq length: 200000000
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Searched:

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TATALIZE M., Fukazawa C.;

Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.

-!- SUBUNIT: Hexamer; each subunit is composed of an acidic and a basic chain derived from a single precursor and linked by a disulfide bond (BY similarity).

-!- SIMILARITY: Belongs to the 11S seed storage protein (globulins)
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
NCBI_TaxID=3848;
                                                                                                  SECUENCE FROW N.A.
MEDLINE=95241635; PubMed=7724684;
Weng W.M., Gao X.S., Zhuang N.L., Xu M.L., Xue Z.T.;
Weng Y.M., Gao X.S., Zhuang N.L., Xu M.L., Xue Z.T.;
The glycinin A3B4 mRNA from wild soybean Glycine soja Sieb. et
"The glycinin A3B4 mRNA from wild soybean Glycine soja Sieb. et
Pauct.";
Plant Physiol. 107:665-666(1995).
-!- SUBVINT: Hexamer; each subunit is composed of an acidic and a
basic chain derived from a single precursor and linked by a
disulfide bond (By similarity).
-!- SIMILARITY: Belongs to the 11S seed storage protein (globulins)
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0
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PRINTS; PR00439; 118GLOBULIN.
PROSITE; PS00305; 118 SEDS STORAGE; 1.
SEG SECONS PROTEIN; Storage protein.
SEQUENCE 517 AA; 58187 MW; 0440F44C72181B7C CRC64;
                                                                                                                                                                                                                                                                                                                                           EMBL, X79467; CAA55977.1; -.
PIR; PQ0807; PQ0806.
PIR; PQ0807; PQ0807.
PIR; PQ08087; PQ0808.
HSSP, PQ4776; JEXZ.
GO; GO:0045735; F:nutrient reservoir activity; IEA.
InterPro; IPR00113; Cupin.
InterPro; IPR011051; RmlC_like_cupin.
InterPro; IPR011051; RmlC_like_cupin.
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HSSP, PO4776; IFXZ.
GO; GO:0045735; F:nutrient reservoir activity; IEA.
InterPro; IPR00045; Cupin.
InterPro; IPR00113; Cupin. region.
InterPro; IPR011051; RmlC like cupin.
InterPro; IPR00164; Seedstore_118.
Pfam; PF00190; Cupin; 2.
PRINTS; PR00439; 11SGLOBULIN.
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Last sequence update)
Last annotation update)
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Best Local Similarity 100.
Matches 9; Conservative
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Fabales; Fabaceae; Papilionoldeae; Phaseoleae; Glycine.
NCBI_TaxID=3847;
                                                                                                                                               Gaps
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MEDLINE-92393391; PubMed=2485233;
MEDLINE-923939191; PubMed=2485233;
Mielsen N.C., Dickinson C.D., Cho T.J., Thanh V.H., Scallon B.J.,
Fischer R.L., Sims T.L., Drews G.N., Goldberg R.B.;
"Characterization of the glycinin gene family in soybean.";
Plant Cell 1:313-328 (1989).
-1- SUBUNIT: Hexamer; each subunit is composed of an acidic and a basic chain derived from a single precursor and linked by a disulfide bond (By similarity).
-1- SIMILARITY: Belongs to the 11S seed storage protein (globulins) family.
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                                                                                             Length 517;
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HSSP; P04776; IFXZ.

GO; GO:0045735; F:nutrient reservoir activity; IEA.

R InterPro; IPR006045; Cupin.

R InterPro; IPR0011051; RmlC like cupin.

R InterPro; IPR00190; Cupin, Seedstore_11s.

R Pfan; PF00190; Cupin, 2.

R PRINTS; PR00439; 11SGLOBULIN.

R PROSITE; PS00305; 11S SEED STORAGE; 1.

SEQUENCE 560 AA; 63679 WW; P95DBEA4012DA024 CRC64;
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PROSITE; PS00105; 11S_SEED_STORAGE; 1.
Seed storage protein; Storage protein.
SEQUENCE 517 AA; 58229 MW; 0EIF51BC72181B7C CRC64;
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Last sequence update)
Last annotation update)
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                                                                                                100.0%; Score 58; DB 2;
100.0%; Pred. No. 0.71;
Live 0; Mismatches
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Name=Gy4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 IPPGVPYWT
                                                                                                                                                                                                        1 IPPGVPYWT
                                                                                                                               Local Similarity
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Pfam; PF00190; Cupin; 2.
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                                                                                            1 IPPGVPYWT
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                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                           NCBI_TaxID=3847;
                                                                                                                                                                                                                                                                                                          TISSUE=Leaves;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=LelB161;
                                                                                                                                                                                                                                                                                                                                                                                     tamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Fragment)
                                                                                                               149
                                                                                                                                                                                                                        Glycinin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 043672;
                                                                                                                                                                                Q9SB11;
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Glycine soja (Wild soybean).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
                                                                                                        Hue Z.T.; Submitted (MAR-1990) to the EMBL/GenBank/DDBJ databases.
-!- SUBUNIT: Hexamer; each subunit is composed of an acidic and a basic chain derived from a single precursor and linked by a disulfide bond (By similarity).
-!- SIMILARITY: Belongs to the 11S seed storage protein (globulins)

    -!- SIMILARITY: Belongs to the l1S seed storage protein (globulins)

                                Xue Z.T., Xu M.L., Shen W., Zhuang N.L., Hu W.M., Shen S.C.; "Characterization of the Gy4 Glycine gene from soybean Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
-!- SUBMYIT: Hexamer; each subunit is composed of an acidic and basic chain derived from a single precursor and linked by a disulfide bond (By similarity).
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                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 58; DB 2; Length 562;
                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                3A4EF28E448AB15A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HISSP, PO4776; IFXZ.
GO; GO:0045735; F:nutrient reservoir activity; IEA.
InterPro; IPR006045; Cupin.
InterPro; IPR011051; Rimic like cupin.
InterPro; IPR0106044; SeedStore_118.
                                                                                                                                                                              EMBL; X52863; CAA37044.1; -.
PIR; PQ0199; P00199.
HR; S20946; S20946.
HSSP; P004776; ERXZ.
GO; GO:0045735; P:nutrient reservoir activity; IEA.
InterPro; IPR0106045; Cupin.
InterPro; IPR01051; Ran Cike cupin.
InterPro; IPR01051; Ran Cike cupin.
                                                                                                                                                                                                                                                                                                                                                               Pred. No. 0.77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      563 AA
                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                            Potential.
                                                                                                                                                                                                                                                                           PRINTS; PR00439; 11SGLOBULIN.
PROSITE; PS00305; 11S_SEED_STORAGE; 1.
                                                                                                                                                                                                                                                                                                                     glycinin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                        MEDLINE=92256811; PubMed=1316192;
                                                               Plant Mol. Biol. 18:897-908(1992)
                                                                                                                                                                                                                                                                                                                                63876 MW;
                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X86970; CAA60533.1; -.
                                                                                                                                                                                                                                                                                                                                                                           9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                 Pfam; PF00190; Cupin; 2
                                                                                                                                                                                                                                                                                                                      562
                                                                                                                                                                                                                                                                                                                                                                                                                  148 iPPGVPYWT 156
                                                                                                                                                                                                                                                                                                                                                                                               1 IPPGVPYWT 9
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                                                                                                                                                                                                                                                                                                                     24 5
562 AA;
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Best Local Similarity
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                                                                                   SEQUENCE FROM N.A.
    SEQUENCE FROM N.A.
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                                                                                               'ISSUE=Leaf;
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                                                      Forrest."
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Vicia.

NCBI_TaxID=3906;
                                                                                                                                                                                                 Gaps
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-!- SUBUNIT: Hexamer; each subunit is composed of an acidic and a basic chain derived from a single precursor and linked by a disulfide bond (By similarity).

-!- SIMILARITY: Belongs to the 11S seed storage protein (globulins)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycine max (Soybean).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids
Spermatophyta, Magnoliophyta, Papilonoideae, Phaseoleae, Glycine.
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                                                                                                                      Query Match
Best Local Similarity 100.0%; Pred. No. 0.78;
Matches 9; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Score 50; DB 2; Length 563;
Best Local Similarity 100.0%; Pred. No. 0.70;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Created)
1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Legumin, legumin-related high molecular weight polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PÉAM; PF00190; Cupin; 2.
PRINTS; PR00439; 11SGLOBULIN:
PROSITE; PS00305; 11S SEDS STORAGE; 1.
SEQUENCE 563 AA; 63797 WW; 4ACC765C55AB9E18 CRC64;
PRINTS; PR00439; ILSGLOBULIN.
PROSITE; PS00305; ILS SEED STORAGE; 1.
SEQUENCE 563 AA; 63806 MW; BC171BED5F2B361F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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PIR, PQ0199; PQ0199.
HSSP; P04776; IFXZ.
GO, GO:0045735; Finitrient reservoir activity; IEA.
InterPro; IPR006045; Cupin.
InterPro; IPR011051; RmlC_like_cupin.
InterPro; IPR006044; Seedstore_lis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  563 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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98.3%;
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01-MAR-2001 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
Glycinin subunit G7.
Query Match
Best Local Similarity 88.3
-Log 8; Conservative
                                                                                                                                                                                                                                                     PRELIMINARY;
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142 IPPGIPYWT 150
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TISSUE-Cotelydon;
                                                                                                 1 IPPGVPYWT
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                                                                                                                                                                                                                                                                                024294;
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ID Q9
AC Q9
DT 01
DT 01
DE Q1
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MEDLINE-94272010; PubMed-8003694;
MEDLINE-94272010; PubMed-8003694;
MEDLINE-94272010; PubMed-8003694;
Heim U., Baeumlein H., Wobus U.;
Heim U., Baeumlein H., Wobus U.;
Plant Wol. Biol. 25:131-135(1994).
-1-SUBMINIT Hexamer; each subunit is composed of an acidic and a basic chain derived from a single precursor and linked by a disulfide bond (By similarity).
-1-SIMILARITY: Belongs to the 11S seed storage protein (globulins)
                                                    TISSUE=Cotyledons, PubMed=8003694; MEDLINE=94572010; PubMed=8003694; MEDLINE=94572010; PubMed=8003694; Heim U., Bacumlain H., Wobus U.; Heim U., Bacumlain gene family: a reconstructed Vicia faba legumin gene encoding a hig-molecular-weight subunit is related to type B genes."; Plant Mol. Biol. 25:131-135(1994). EMBL; Z26487; CAAB1261.1; -. PIR; T12140; T12140.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=LelB3;
Vicia faba (Broad bean).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
Spermatophyta; Magnoliophyta; eudicotyledons; Vicieae; Vicia.
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01-NAR-2004 (TrEMBLrel. 26, Last annotation update)
Legumin; legumin-related high molecular weight polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                 98.3%; Score 57; DB 2; Length 136; 88.9%; Pred. No. 0.26; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64502 MW; 568E497245A1915A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Z2648; CAA81262.1; -.
PIR; $46503; $37241.
HSSP: P04776; IPXZ.
GO; GO:04735; F:nutrient reservoir activity; IEA.
GO; GO:04735; F:nutrient reservoir activity; IEA.
InterPro; IPR0007113; Cupin_region.
InterPro; IPR00077; DNA ligase.
InterPro; IPR01051; RmlC like cupin.
InterPro; IPR01051; RmlC like cupin.
PROSITE; PS00190; Cupin; 2.
PRINTS; PR00439; 11SGTOBULIN.
PROSITE; PS000597; DNA LIGASE A1; UNKNOWN 1.
Seed storage protein; Signal; Storage protein.
                                                                                                                                                                                                                                                                                                                                                                                           136 AA; 15317 MW; 3C24820F2630F069 CRC64;
                                                                                                                                                                                                          PIR; T12140; T12140.
HSSP; P04776; IFXZ.
GOG; GO:0045735; F:nutrient reservoir activity; IEA.
InterPro; IPR006045; Cupin.
InterPro; IPR007113; Cupin. region.
InterPro; IPR010151; RmlC_IIke_cupin.
PF00190; Cupin; 1.
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Matches 8; Conservative
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|PPGIPYWT 58
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                                  SEQUENCE FROM N.A.
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                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bown D.P.;
Submitted (JUN-1992) to the EMBL/GenBank/DDBJ databases.
Submitted (JUN-1992) to the EMBL/GenBank/DDBJ databases.
--- SUBUNIT: Hexamer; each subunit is composed of an acidic and a basic chain derived from a single precursor and linked by a disulfide bond (By similarity).
--- SIMILMARITY: Belongs to the 11S seed storage protein (globulins) family.
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Pred. No. 1.1;
1; Mismatches 0; Indels
Score 57; DB 2; Length 564;
Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUB-Cotelydon;
Bown D.O., Gatehouse J.A.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                         Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        566 AA; 64872 MW; 663A80DE265359CE CRC64;
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Last annotation update)
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01-7AN-1998 (TrEMBLrel. 05, Created)
01-7AN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, X6424; CRA47809.1; -.
PIR; T06453; T06453.
HSSP; P04776; 1FXZ.
GO; GO:0045735; F:nutrient reservoir activity; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR006045; Cupin.
InterPro; IPR007113; Cupin.
InterPro; IPR000777; DNA ligase.
InterPro; IPR001097; DNA ligase.
InterPro; IPR011051; RmlC like cupin.
InterPro; IPR001091; Cupin. 2.
PRINTS; PR004139; 115G109UJIN.
PROSITE; PS00439; 115G109UJIN.
PROSITE; PS00497; DNA LIGASE A1, UNKNOWN 1.
Seed storage protein; Signal; Storage protein.
SIGNAL
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                                                               1; Mismatches
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                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                    Legumin (Minor small) precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98.3%;
88.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=legS;
Pisum sativum (Garden pea).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 88.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Phaseoleae, Glycine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disulfide bond.
-!- SIMILARITY: Belongs to the 11S seed storage protein (globulins)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam, PF00190; Cupin; 2.
PRINTS; PR00439; 11SGLOBULIN.
PROSITE; PS00305; 11S_SEED_STORAGE; 1.
Direct protein sequencing; Multigene family; Seed storage protein;
                                                                                                                                                                                                                                                            STRAIN=cv. Bonminori;
Hirano H., Fukazawa C., Harada K.;
Hirano H., Fukazawa C., Harada K.;
"The primary structures of the A4 and A5 subunits are highly homologous to the A3 subunit in the glycinin seed storage protein of soybean.";
FEBS Lett. 181:124-128 (1985).
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 181-386 FROM N.A. STRAIN=cv. CX635-1-1-1; Scallon B.J., Dickinson C.D., Nielsen N.C.; "Characterization of a null-allele for the Gy4 glycinin gene from
                                                                                                 SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-C.V. Bornhinori,
MEDIJNE-85230643; PubMed=2988947;
MORMMA T., Negoro T., Hirano H., Matsumoto A., Udaka K., Fukazawa
Mormma T., Negoro T., Hirano H., Matsumoto A., Udaka K., Fukazawa
"Glycinin A5A483 mRNA: cDNA cloning and nucleotide sequencing of
splitting storage protein subunit of soybean.";
Eur. J. Biochem. 149:491-496(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycinin A5 subunit.
Glycinin A4 subunit.
Glycinin B3 subunit.
Interchain B9 subunit.
L -> F (in Ref. 2).
S -> L (in Ref. 2).
I -> V (in Ref. 2).
I -> V (in Ref. 2).
I -> Y (in Ref. 2).
I -> Y (in Ref. 2).
I -> Y (in Ref. 2).
E -> Q (in Ref. 3).
NKTG -> EQDQD (in Ref. 3).
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Pred. No.
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EMBL, X05622; CAB57802.1; -.
PIR, A91145; FWSYGS.
HSSP, P04776; 1FXZ.
HIACEPPO; IPRO6045; Cupin.
InterPro; IPRO11051; RMLC like cupin.
InterPro; IPRO106044; Seed@tore_118.
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377
384
384
29
82
86
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Glycine max (Soybean)
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105
117
253
332
562 AA;
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Best Local Similarity
                                                                   NCBI_TaxID=3847;
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SIGNAL
CHAIN
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
NCBI_TaxID=3847;
          Glycine max (Soybean).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
NCBL_TaxID=3847;
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Last annotation update)
[Contains: Glycinin A5 subunit; Glycinin A4
                                                                                                                         SEQUENCE FROM N.A.
Beilinson V., Chen Z., Shoemaker R.C., Fischer R.L., Goldberg R.B.
Nielsen N.C.;
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY649099; AAT68239.1; -
SEQUENCE 536 AA; 60514 MW; 94EF37198D1C4468 CRC64;
                                                                                                                                                                                                                                                          GO, GO:0045735; F:nutrient reservoir activity; IEA.
InterPro; IPR00645; Cupin.
InterPro; IPR01113; Cupin.
InterPro; IPR011051; RmlC_like.cupin.
InterPro; IPR010604; SeedStore_lis.
Pfam; PF00190; Cupin, 2.
PRINTS; PR00439; IISGLOBULIN.
SEQUENCE 536 AA; 60486 MW; 40F452FAA067FBC7 CRC64;
                                                                                                                                                                    "Genomic organization of glycinin genes in soybean.";
Theor. Appl. Genet. 104:1132-1140(2002).
EMBL; AF319777; AAG42489.1; -.
EMBL; AF319776; AAG42488.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    536 AA.
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Local Similarity 77.8%; Pred. No. 1.5;
1es 7; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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13-AUG-1987 (Rel. 05, Last seq
05-JUL-2004 (Rel. 4, Last ann
Glycinin G4 precursor (Containn
subunit; Glycinin B3 subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2004 (TrEMBLrel. 28, 01-OCT-2004 (TrEMBLrel. 28, 01-OCT-2004 (TrEMBLrel. 28, Glycinin subunit G7.
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137 VPPGIPYWT 145
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137 VPPGIPYWT 145
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P02858;
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Search completed: November 6, 2004, 19:52:53
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05-JUL-2004 (Rel. 44, Last annocation update)
Legumin type B precursor [Contains: Legumin type B acidic chain); Legumin type B beta chain (Legumin type B basic chain);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=86176760; PubMed=3960730; MEDLINE=86176760; PubMed=3960730; Baeunhlein H., Wobus U., Pustell J., Kafatos F.C.; Baeunhlein H., Wobus U., Pustell J., Laructure of a B type gene of Vicia faba and a possible legumin gene specific regulatory element."; Nucleic Acida Res. 14:270-2720(1986).

-I-FUNCTION: This protein found in the seeds of many leguminous and nonleguminous plants is the source of sulfur-containing amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
  Gaps
                                                                                                                                                                                                                                                                                                                          Vicinate faba (Broad bean).

Sukaryota, faraha (Broad bean).

Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids I; Fabales, Fabaceae, Papilionoideae, Vicieae, Vicia.

NCBI_TaxID=3906,
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    Indels
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  0; Mismatches
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Vicia faba (Broad bean).
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    8; Conservative
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                                              1 IPPGVPYWT 9
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Les 7; Conserv
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ID LEG4 VICFA
AC P05190;
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Matches
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      Matches
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                SUBUNIT: Hexamer; each subunit is composed of an acidic and a basic chain derived from a single precursor and linked by a disulfide bond.
SIMILARITY: Belongs to the 11S seed storage protein (globulins)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Legumin type B alpha chain.
Legumin type B beta chain.
Interchain (alpha-beta) (Potential).
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                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR006045; Cupin.
InterPro; IPR007113; Cupin. region.
InterPro; IPR011051; RmlC_like_cupin.
InterPro; IPR006044; Seedstore_lls.
Pfam; PF00190; Cupin; 2.
PRINTS; PR00439; 11SGLOBULIN.
PRINTS; PR00305; 11S SEED_STORAGE; 1.
Multigene family; Seed storage protein; Signal.
SIGNAL
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Pred. No. 18;
1; Mismatches
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Gln/Glu-rich.
Gln/Glu-rich.
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7; Conservative
acids in seed meals.
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                                                                                                                family.
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DOMAIN
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SEQUENCE
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